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*M. Basco*

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/030,482B

DATE: 04/26/2001  
TIME: 11:56:25

Input Set : D:\38109-20007.00 seqlist (final)!.txt  
Output Set: N:\CRF3\04262001\I030482B.raw

P.S

4 <110> APPLICANT: Snutch, Terry  
5 NeuroMed Technologies, Inc.  
7 <120> TITLE OF INVENTION: NOVEL HUMAN CALCIUM CHANNELS AND RELATED  
8 PROBES, CELL LINES AND METHODS  
11 <130> FILE REFERENCE: 38109-20007.00  
13 <140> CURRENT APPLICATION NUMBER: US 09/030,482B  
14 <141> CURRENT FILING DATE: 1998-02-25  
16 <150> PRIOR APPLICATION NUMBER: US 60/039,204  
17 <151> PRIOR FILING DATE: 1997-02-28  
19 <160> NUMBER OF SEQ ID NOS: 33  
21 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
23 <210> SEQ ID NO: 1  
24 <211> LENGTH: 24  
25 <212> TYPE: DNA  
26 <213> ORGANISM: Rat  
28 <400> SEQUENCE: 1  
29 gtcaaaaactc aggccattcta ctgg 24  
31 <210> SEQ ID NO: 2  
32 <211> LENGTH: 24  
33 <212> TYPE: DNA  
34 <213> ORGANISM: Rat  
36 <400> SEQUENCE: 2  
37 aacgtgttct tggctatcgc ggtg 24  
39 <210> SEQ ID NO: 3  
40 <211> LENGTH: 24  
41 <212> TYPE: DNA  
42 <213> ORGANISM: Rat  
44 <400> SEQUENCE: 3  
45 gtgaaagcac agagcttcta ctgg 24  
47 <210> SEQ ID NO: 4  
48 <211> LENGTH: 24  
49 <212> TYPE: DNA  
50 <213> ORGANISM: Rat  
52 <400> SEQUENCE: 4  
53 aacgttttct tggccattgc tgtg 24  
55 <210> SEQ ID NO: 5  
56 <211> LENGTH: 24  
57 <212> TYPE: DNA  
58 <213> ORGANISM: Rat  
60 <400> SEQUENCE: 5  
61 gttaaatcca acgtcttcta ctgg 24  
63 <210> SEQ ID NO: 6  
64 <211> LENGTH: 24  
65 <212> TYPE: DNA  
66 <213> ORGANISM: Rat  
68 <400> SEQUENCE: 6  
69 aatgtgttct tggccattgc ggtg 24

ENTERED

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71 <210> SEQ ID NO: 7
72 <211> LENGTH: 24
73 <212> TYPE: DNA
74 <213> ORGANISM: Rat
76 <400> SEQUENCE: 7
77 gtgaagtctg tcacgttta ctgg 24
79 <210> SEQ ID NO: 8
80 <211> LENGTH: 24
81 <212> TYPE: DNA
82 <213> ORGANISM: Rat
84 <400> SEQUENCE: 8
85 aagctttct tggccattgc tgta 24
87 <210> SEQ ID NO: 9
88 <211> LENGTH: 24
89 <212> TYPE: DNA
90 <213> ORGANISM: Rat
92 <400> SEQUENCE: 9
93 gtcaagtcgc aagtgttcta ctgg 24
95 <210> SEQ ID NO: 10
96 <211> LENGTH: 24
97 <212> TYPE: DNA
98 <213> ORGANISM: Rat
100 <400> SEQUENCE: 10
101 aatgtattct tggctatcgc tgtg 24
103 <210> SEQ ID NO: 11
104 <211> LENGTH: 21
105 <212> TYPE: DNA
106 <213> ORGANISM: Rat
108 <400> SEQUENCE: 11
109 atctaygcyr tsatyggsat g 21
111 <210> SEQ ID NO: 12
112 <211> LENGTH: 20
113 <212> TYPE: DNA
114 <213> ORGANISM: Rat
116 <400> SEQUENCE: 12
117 atggacaayt tygastaytc 20
119 <210> SEQ ID NO: 13
120 <211> LENGTH: 168
121 <212> TYPE: DNA
122 <213> ORGANISM: Human
124 <220> FEATURE:
125 <223> OTHER INFORMATION: Expressed sequence tag H55225
127 <400> SEQUENCE: 13
128 gtgatcactc tggaggctg ggtggagatc atgtactacg tggatggatgc tcactccttc 60
129 tacaacttca tctacttcat cctgcttatac ataccctct tgccttgac cccatatgg 120
130 cttcccaagag tgagctcatc cacctcgtca tgcctgactc gacgttca 168
132 <210> SEQ ID NO: 14
133 <211> LENGTH: 98
134 <212> TYPE: DNA
  
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135 <213> ORGANISM: Human  
 137 <220> FEATURE:  
 138 <223> OTHER INFORMATION: Expressed sequence tag H55617  
 140 <400> SEQUENCE: 14  
 141 gatggtcgag tactccctgg accttcagaa catcaacctg tcagccatcc gcaccgtgcg 60  
 142 cgtcctgagg cccctcaaag ccatcaaccg cgtgccca 98  
 144 <210> SEQ ID NO: 15  
 145 <211> LENGTH: 94  
 146 <212> TYPE: DNA  
 147 <213> ORGANISM: Human  
 149 <220> FEATURE:  
 150 <223> OTHER INFORMATION: Expressed sequence tag H55223  
 152 <400> SEQUENCE: 15  
 153 catgctgggt atcctgctga actgcgtgac acttggcatg taccagccgt gcgacgacat 60  
 154 ggactgcctg tccgaccgct gcaagatcct gcag 94  
 156 <210> SEQ ID NO: 16  
 157 <211> LENGTH: 123  
 158 <212> TYPE: DNA  
 159 <213> ORGANISM: Human  
 161 <220> FEATURE:  
 162 <223> OTHER INFORMATION: Expressed sequence tag H55544  
 164 <400> SEQUENCE: 16  
 165 gatatctctgg ttacttttagt agccaaacact cttggctact cagacccctgg tcccatataaa 60  
 166 tccctgcgaa ccttgagagc actaagacct ctaagagctt tgtctagatt tgaaggaatg 120  
 167 agg 123  
 169 <210> SEQ ID NO: 17  
 170 <211> LENGTH: 343  
 171 <212> TYPE: DNA  
 172 <213> ORGANISM: Human  
 174 <220> FEATURE:  
 175 <223> OTHER INFORMATION: Expressed sequence tag F07776  
 177 <221> NAME/KEY: misc\_feature  
 178 <222> LOCATION: (1)...(343)  
 179 <223> OTHER INFORMATION: n = A,T,C or G  
 181 <400> SEQUENCE: 17  
 182 ttctctccat tggatggatg tttctggctg aactgataga aaagtatttt gtgtgcccta 60  
 W--> 183 cccctgttncg agtgatccgt cttgccagga ttggccgaat cctacgtctg atcaaaggag 120  
 184 caaaggggat ccgcacgctg ctctttgcctt tgatgatgtc cttccctgcg ttgtttaaca 180  
 W--> 185 tcgggnctccct tcttttcctg gtcatgttca tctacgnat ctttggatg tccaaatttg 240  
 W--> 186 cctatgttaa gagggaaatgg gggatcgatg acatgttnan ctttggatcacc tttggcaaca 300  
 187 gcatgatctg cctgttccaa attacaacct ctgctggctg gga 343  
 189 <210> SEQ ID NO: 18  
 190 <211> LENGTH: 5562  
 191 <212> TYPE: DNA  
 192 <213> ORGANISM: Human  
 194 <220> FEATURE:  
 195 <221> NAME/KEY: CDS  
 196 <222> LOCATION: (1)...(5562)  
 197 <223> OTHER INFORMATION: Human alpha-1 partial sequence from BAC bK206c7

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199 <400> SEQUENCE: 18  
 200 atg ttt ttc gtc tca gcc aat ccc tgg gtg agt ttc acc agt ttt gat 48  
 201 Met Phe Phe Val Ser Ala Asn Pro Trp Val Ser Phe Thr Ser Phe Asp  
 202 1 5 10 15  
 204 tta aac gtg gcc aat atg gac aac ttc ttc gcc ccc gtt ttc acc atg 96  
 205 Leu Asn Val Ala Asn Met Asp Asn Phe Phe Ala Pro Val Phe Thr Met  
 206 20 25 30  
 208 ggc aaa tat tat acg cca ggc gac aag gtg ctg atg ccg ctg gcg att 144  
 209 Gly Lys Tyr Tyr Thr Gln Gly Asp Lys Val Leu Met Pro Leu Ala Ile  
 210 35 40 45  
 212 cag gct ctg aaa cag ctg atg ttc aaa ttg gtg gcc act gtt gct cga 192  
 213 Gln Ala Leu Lys Gln Leu Met Phe Lys Leu Val Ala Thr Val Ala Arg  
 214 50 55 60  
 216 aca cat gct aca ccg tca cac atc acg ggt ggt cct gga aca ggg atg 240  
 217 Thr His Ala Thr Pro Ser His Ile Thr Gly Gly Pro Gly Thr Gly Met  
 218 65 70 75 80  
 220 cac acg ggc acc ttc cag gaa gga gct gag cct ggt tca tct cag cac 288  
 221 His Thr Gly Thr Phe Gln Glu Gly Ala Glu Pro Gly Ser Ser Gln His  
 222 85 90 95  
 224 cct gag gca cag gcc acg tat aca gca ggg tgc acc cca gcc ccc acg 336  
 225 Pro Glu Ala Gln Ala Thr Tyr Thr Ala Gly Cys Thr Pro Ala Pro Thr  
 226 100 105 110  
 228 ggc gat ccc acc tgc tgc ttt gtc ctt gac ttg gtg tgc acg tgg ttt 384  
 229 Gly Asp Pro Thr Cys Cys Phe Val Leu Asp Leu Val Cys Thr Trp Phe  
 230 115 120 125  
 232 gaa tgt gtc agc atg ctg gtg atc ctg ctg aac tgc gtg aca ctt ggc 432  
 233 Glu Cys Val Ser Met Leu Val Ile Leu Leu Asn Cys Val Thr Leu Gly  
 234 130 135 140  
 236 atg tac cag ccg tgc gac gac atg gac tgc ctg tcc gac cgc tgc aag 480  
 237 Met Tyr Gln Pro Cys Asp Asp Met Asp Cys Leu Ser Asp Arg Cys Lys  
 238 145 150 155 160  
 240 atc ctg cag gtc ttt gat gac ttc atc ttt atc ttc ttt gcc atg gag 528  
 241 Ile Leu Gln Val Phe Asp Asp Phe Ile Phe Ile Phe Ala Met Glu  
 242 165 170 175  
 244 atg gtg ctc aag atg gtg gcc ctg ggg att ttt ggc aag aag tgc tac 576  
 245 Met Val Leu Lys Met Val Ala Leu Gly Ile Phe Gly Lys Lys Cys Tyr  
 246 180 185 190  
 248 ctc ggg gac aca tgg aac cgc ctg gat ttc ttc atc gtc atg gca ggc 624  
 249 Leu Gly Asp Thr Trp Asn Arg Leu Asp Phe Phe Ile Val Met Ala Gly  
 250 195 200 205  
 252 aac atc aac ctg tca gcc atc cgc acc gtg cgc gtc ctg agg ccc ctc 672  
 253 Asn Ile Asn Leu Ser Ala Ile Arg Thr Val Arg Val Leu Arg Pro Leu  
 254 210 215 220  
 256 aaa gcc atc aac cgc gtg ccc agt atg cgg atc ctg gtg aac ctg ctc 720  
 257 Lys Ala Ile Asn Arg Val Pro Ser Met Arg Ile Leu Val Asn Leu Leu  
 258 225 230 235 240  
 260 ctg gac aca ctg ccc atg ctg ggg aat gtc ctg ctg ctc tgc ttc ttt 768  
 261 Leu Asp Thr Leu Pro Met Leu Gly Asn Val Leu Leu Cys Phe Phe  
 262 245 250 255

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264 gtc ttc ttc atc ttt ggc atc ata ggt gtg cag ctc tgg gcg ggc ctg	816
265 Val Phe Phe Ile Phe Gly Ile Ile Gly Val Gln Leu Trp Ala Gly Leu	
266 260 265 270	
268 ctg cgt aac cgc tgc ttc ctg gag gag aac ttc acc ata caa ggg gat	864
269 Leu Arg Asn Arg Cys Phe Leu Glu Glu Asn Phe Thr Ile Gln Gly Asp	
270 275 280 285	
272 gtg gcc ttg ccc cca tac tac cag ccg gag gag gat gat gag atg ccc	912
273 Val Ala Leu Pro Pro Tyr Tyr Gln Pro Glu Glu Asp Asp Glu Met Pro	
274 290 295 300	
276 ttc atc tgc tcc ctg tcg ggc gac aat ggg ata atg ggc tgc cat gag	960
277 Phe Ile Cys Ser Leu Ser Gly Asp Asn Gly Ile Met Gly Cys His Glu	
278 305 310 315 320	
280 atc ccc ccg ctc aag gag cag ggc cgt gag tgc tgc ctg tcc aag gac	1008
281 Ile Pro Pro Leu Lys Glu Gln Gly Arg Glu Cys Cys Leu Ser Lys Asp	
282 325 330 335	
284 gac gtc tac gac ttt ggg gcg ggg cgc cag gac ctc aat gcc agc ggc	1056
285 Asp Val Tyr Asp Phe Gly Ala Gly Arg Gln Asp Leu Asn Ala Ser Gly	
286 340 345 350	
288 ctc tgt gtc aac tgg aac cgt tac tac aat gtg tgc cgc acg ggc agc	1104
289 Leu Cys Val Asn Trp Asn Arg Tyr Tyr Asn Val Cys Arg Thr Gly Ser	
290 355 360 365	
292 gcc aac ccc cac aag ggt gcc atc aac ttt gac aac atc ggt tat gct	1152
293 Ala Asn Pro His Lys Gly Ala Ile Asn Phe Asp Asn Ile Gly Tyr Ala	
294 370 375 380	
296 tgg att gtc atc ttc cag gtg atc act ctg gaa ggc tgg gtg gag atc	1200
297 Trp Ile Val Ile Phe Gln Val Ile Thr Leu Glu Gly Trp Val Glu Ile	
298 385 390 395 400	
300 atg tac tac gtg atg gat gct cac tcc ttc tac aac ttc atc tac ttc	1248
301 Met Tyr Tyr Val Met Asp Ala His Ser Phe Tyr Asn Phe Ile Tyr Phe	
302 405 410 415	
304 atc ctg ctt atc ata agt gag ctc atc cac ctc gtc atg cct gac tgc	1296
305 Ile Leu Leu Ile Ile Ser Glu Leu Ile His Leu Val Met Pro Asp Cys	
306 420 425 430	
308 agc ttc agc aca gca cag tcc cca aaa tgt caa ggt gat tca ctc cca	1344
309 Ser Phe Ser Thr Ala Gln Ser Pro Lys Cys Gln Gly Asp Ser Leu Pro	
310 435 440 445	
312 gga gtc gct gaa tcc ctg ctg ctg cga gac tct agc tcc tca gtc	1392
313 Gly Val Ala Ala Glu Ser Leu Leu Leu Arg Asp Ser Ser Ser Val	
314 450 455 460	
316 atc act gat gag gct gca gcc atg gag aac ctc ctg gcg ggc acc tcc	1440
317 Ile Thr Asp Glu Ala Ala Met Glu Asn Leu Leu Ala Gly Thr Ser	
318 465 470 475 480	
320 aag ggg gat gaa agc tat ctg ctc agg ctg gcc ggc agc caa gtt cac	1488
321 Lys Gly Asp Glu Ser Tyr Leu Leu Arg Leu Ala Gly Ser Gln Val His	
322 485 490 495	
324 tcc cag gct cag caa atg ctg ggg agg ggg ctg ggc cct gaa agc ctg	1536
325 Ser Gln Ala Gln Gln Met Leu Gly Arg Gly Leu Gly Pro Glu Ser Leu	
326 500 505 510	
328 gaa act gga gag gag ccc cac tcg tgg agc cct cgg gcc aca agg aga	1584

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

**VERIFICATION SUMMARY**

PATENT APPLICATION: US/09/030,482B

DATE: 04/26/2001

TIME: 11:56:26

Input Set : D:\38109-20007.00 seqlist (final)!.txt  
Output Set: N:\CRF3\04262001\I030482B.raw

L:183 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17  
L:185 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17  
L:186 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17  
L:1198 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33